1655

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/664,827_

Source: _OIPE_

Date Processed by STIC: _9/26/2000_
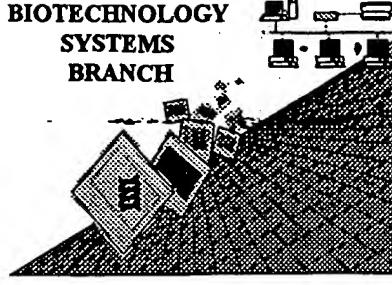
RECEIVED
JAN 24 2001
TECH CENTER 1600/29

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,

2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR FURTHER INFORMATION, PLEASE TELEPHONE MARK SPENCER, 703-308-4212.

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

<u>Checker Version 3.0 can be down loaded from the USPTO website at the following address:</u>
http://www.uspto.gov/web/offices/pac/checker

```
RAW SEQUENCE LISTING                    DATE: 09/26/2000
PATENT APPLICATION:   US/09/664,827     TIME: 12:03:32

Input Set : A:\SeqList.txt
Output Set: N:\CRF3\09262000\I664827.raw
```

**Does Not Comply
Corrected Diskette Needed**

```
     3 <110> APPLICANT: Erikson, Glen
     5 <120> TITLE OF INVENTION: QUADRUPLEX DNA SYSTEM
     7 <130> FILE REFERENCE: E1047/20044
     9 <140> CURRENT APPLICATION NUMBER: US/09/664,827
     9 <141> CURRENT FILING DATE: 2000-09-19
     9 <160> NUMBER OF SEQ ID NOS: 15
    11 <170> SOFTWARE: PatentIn version 3.0
    13 <210> SEQ ID NO: 1
    14 <211> LENGTH: 50
    15 <212> TYPE: DNA
    16 <213> ORGANISM: synthetic construct
    18 <400> SEQUENCE: 1
    19 gagcaccatg acagacactg tcatctctgg tgtgtcctac gatgactctg        50
    22 <210> SEQ ID NO: 2
    23 <211> LENGTH: 50
    24 <212> TYPE: DNA
    25 <213> ORGANISM: synthetic construct
    27 <400> SEQUENCE: 2
    28 cagagtcatc gtaggacaca ccagagatga cagtgtctgt catggtgctc        50
    31 <210> SEQ ID NO: 3
    32 <211> LENGTH: 50
    33 <212> TYPE: DNA
    34 <213> ORGANISM: synthetic construct
    36 <400> SEQUENCE: 3
    37 gagcaccatg acagacactg tcgtctctgg tgtgtcctac gatgactctg        50
    40 <210> SEQ ID NO: 4
    41 <211> LENGTH: 50
    42 <212> TYPE: DNA
    43 <213> ORGANISM: synthetic construct
    45 <400> SEQUENCE: 4
    46 cagagtcatc gtaggacaca ccagagacga cagtgtctgt catggtgctc        50
    49 <210> SEQ ID NO: 5
    50 <211> LENGTH: 50
    51 <212> TYPE: DNA
    52 <213> ORGANISM: synthetic construct
    54 <400> SEQUENCE: 5
    55 gagcaccatg acagacactg tcttctctgg tgtgtcctac gatgactctg        50
    58 <210> SEQ ID NO: 6
    59 <211> LENGTH: 50
    60 <212> TYPE: DNA
    61 <213> ORGANISM: synthetic construct
    63 <400> SEQUENCE: 6
    64 cagagtcatc gtaggacaca ccagagaaga cagtgtctgt catggtgctc        50
    67 <210> SEQ ID NO: 7
    68 <211> LENGTH: 50
    69 <212> TYPE: DNA
    70 <213> ORGANISM: synthetic construct
```

per new Sequence Rules, the only valid responses are: Unknown, Artificial Sequence, or Scientific name (Genus/species)

(see circled portion of Item 12 on Error Summary sheet)

global error

OK

RAW SEQUENCE LISTING   DATE: 09/26/2000
PATENT APPLICATION: US/09/664,827   TIME: 12:03:32

Input Set : A:\SeqList.txt
Output Set: N:\CRF3\09262000\I664827.raw

```
 72 <400> SEQUENCE: 7
 73 gagcaccatg acagacactg tcatctttgg tgtgtcctac gatgactctg          50
 76 <210> SEQ ID NO: 8
 77 <211> LENGTH: 50
 78 <212> TYPE: DNA
 79 <213> ORGANISM: synthetic construct
 81 <400> SEQUENCE: 8
 82 cagagtcatc gtaggacaca ccaaagatga cagtgtctgt catggtgctc          50
 85 <210> SEQ ID NO: 9
 86 <211> LENGTH: 50
 87 <212> TYPE: DNA
 88 <213> ORGANISM: synthetic construct
 90 <400> SEQUENCE: 9
 91 gagcaccatg acagacactg tcatccctgg tgtgtcctac gatgactctg          50
 94 <210> SEQ ID NO: 10
 95 <211> LENGTH: 50
 96 <212> TYPE: DNA
 97 <213> ORGANISM: synthetic construct
 99 <400> SEQUENCE: 10
100 cagagtcatc gtaggacaca ccagggatga cagtgtctgt catggtgctc          50
103 <210> SEQ ID NO: 11
104 <211> LENGTH: 15
105 <212> TYPE: DNA
106 <213> ORGANISM: synthetic construct
108 <400> SEQUENCE: 11
109 ctgtcatctc tggtg                                               15
112 <210> SEQ ID NO: 12
113 <211> LENGTH: 15
114 <212> TYPE: DNA
115 <213> ORGANISM: synthetic construct
117 <400> SEQUENCE: 12
118 caccagagat gacag                                               15
121 <210> SEQ ID NO: 13
122 <211> LENGTH: 15
123 <212> TYPE: DNA
124 <213> ORGANISM: synthetic construct
126 <400> SEQUENCE: 13
127 gacagtagag accac                                               15
130 <210> SEQ ID NO: 14
131 <211> LENGTH: 15
132 <212> TYPE: DNA
133 <213> ORGANISM: synthetic construct
135 <400> SEQUENCE: 14
136 gtggtctcta ctgtc                                               15
139 <210> SEQ ID NO: 15
140 <211> LENGTH: 50
141 <212> TYPE: DNA
142 <213> ORGANISM: synthetic construct
144 <400> SEQUENCE: 15
```

```
145 cagagtcatc gtaggacaca ccagcgatga cagtgtctgt catggtgctc          50
```

VERIFICATION SUMMARY   DATE: 09/26/2000
PATENT APPLICATION: US/09/664,827   TIME: 12:03:33

Input Set : A:\SeqList.txt
Output Set: N:\CRF3\09262000\I664827.raw

L:9 M:270 C: Current Application Number differs, Replaced Current Application No
L:9 M:271 C: Current Filing Date differs, Replaced Current Filing Date

Raw Sequence Listing Error Summary

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics   The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos   The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length   The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid   The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
Numbering   between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII   This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length   Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"   A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(OLD RULES)   **(2) INFORMATION FOR SEQ ID NO:X:**
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences   Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
(NEW RULES)   **<210> sequence id number**
<400> sequence id number
000

10 _____ Use of n's or Xaa's   Use of n's and/or Xaa's have been detected in the Sequence Listing.
(NEW RULES)   Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of <213>Organism   Sequence(s) _____ are missing this mandatory field or its response.
(NEW RULES)

12 _____ Use of <220>Feature   Sequence(s) _____ are missing the <220>Feature and associated headings.
(NEW RULES)   Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"   Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.